

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 3, 2002, 02:14:49 : Search time 1766.36 Seconds
(without alignments)
168.104 Million cell updates/sec

Title: US-09-802-359B-1

Perfect score: 22

Sequence: 1 tgactgtgaacctgcgagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estlin:*
- 4: em_estlinu:*
- 5: em_estlov:*
- 6: em_estlpl:*
- 7: em_estro:*
- 8: em_hlc:*
- 9: gd_estl:*
- 10: gb_estl2:*
- 11: gb_hlc:*
- 12: gb_gss:*
- 13: em_gss_hum:*
- 14: em_gss_inu:*
- 15: em_gss_pln:*
- 16: em_gss_vrl:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.4	83.6	571	10	BM042508 603615795
2	17.8	80.9	561	12	AZ755668 ev02g09.x
3	17.8	80.9	961	10	BF971856 602240444
4	17.4	79.1	489	12	AZ060178 RPT-23-4
5	17.4	79.1	530	12	AZ886419 RPT-23-1
6	17.2	78.2	374	12	AQ245026 HS_2036_B
7	17.2	78.2	408	12	AZ536502 110300_96
8	17.2	78.2	424	10	BE723539 193384 MA
9	17.2	78.2	463	9	AU083559 AU083559
10	17.2	78.2	479	9	AU089685 AU089685
11	17.2	78.2	513	10	BJ094274 BJ094274
12	17.2	78.2	519	10	BI796581 BI796581
13	17.2	78.2	571	10	BM037907 BM037907
14	17.2	78.2	972	12	CNS05FPD9 AL347814 Tetradon
15	16.8	76.4	105	9	AA094019 c11619.se
16	16.8	76.4	523	12	AZ483488 IM0309M12
17	16.8	76.4	526	12	AZ501799 IM0340J17

Result No.	Score	Query Match	Length	DB ID	Description
18	16.8	76.4	681	9	AV732648 AV732648
19	16.8	76.4	705	9	AM916461 AM916461
20	16.8	76.4	864	12	BH207673 BH207673
21	16.4	74.5	400	9	AM398307 AM398307
22	16.4	74.5	496	9	AM034934 AM034934
23	16.4	74.5	546	12	AZ058706 AZ058706
24	16.4	74.5	554	12	AZ280611 AZ280611
25	16.4	74.5	599	12	AZ068022 AZ068022
26	16.4	74.5	600	12	AZ976014 AZ976014
27	16.4	74.5	633	10	BG570577 BG570577
28	16.4	74.5	747	10	BG127461 BG127461
29	16.4	74.5	934	12	CNS027SC CNS027SC
30	16.2	73.6	202	9	AA236074 AA236074
31	16.2	73.6	236	9	BB183285 BB183285
32	16.2	73.6	236	10	BP932252 BP932252
33	16.2	73.6	251	9	BB565758 BB565758
34	16.2	73.6	286	9	A1099019 A1099019
35	16.2	73.6	297	9	AA445764 AA445764
36	16.2	73.6	300	10	C11370 C11370
37	16.2	73.6	300	12	AO581066 AO581066
38	16.2	73.6	317	9	BE119339 BE119339
39	16.2	73.6	360	9	AV189436 AV189436
40	16.2	73.6	398	10	BE428418 BE428418
41	16.2	73.6	401	10	BE275964 BE275964
42	16.2	73.6	416	12	AO646593 AO646593
43	16.2	73.6	432	10	BG813145 BG813145
44	16.2	73.6	434	10	BB851024 BB851024
45	16.2	73.6	434	12	BH187088 BH187088

ALIGNMENTS

RESULT 1
LOCUS BM042508 571 bp mRNA linear EST 07-NOV-2001
DEFINITION 603615795F1 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:5420734 3'
ACCESSION BM042508
VERSION BM042508.1 GI:16771788
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE NIH-MGC <http://mgi.ncl.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCM1875 row: m column: 23
High quality sequence start: 44
High quality sequence stop: 411.
Location/Qualifiers
1..571

FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:5420734"
/clone_lib="NIH_MGC_112"
/issue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pORTB7; Site_1: xhoI; Site_2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCGCGAG(G). Library constructed by Ling Hong in the



BASE COUNT 175 a 120 c 139 g 137 t
 ORIGIN NIH_MGC Library " " Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library "

Query Match 83.6%: Score 18.4; DB 10; Length 571;
 Best Local Similarity 95.0%: Pred. No. 1.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgctcgagat 20
 |||||||
 DB 504 TGACTGTGAACGCTTAGAR 523

RESULT 2 A2755668 561 bp DNA linear GSS 01-MAR-2001
 LOCUS ev02909.x1 PAX3 CASTing Library 'ev' Homo sapiens genomic clone
 DEFINITION A2755668 random, DNA sequence.
 ACCESSION A2755668
 VERSION A2755668.1 GI:13175090
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 561)
 AUTHORS Barber,T.D., Barber,M.C., Tomescu,O., Barr,F., Ruben,S. and
 Friedman,T.B.
 TITLE Cyclic amplification and selection of target genes regulated by
 PAX3 and PAX3/FKHR in embryogenesis and alveolar rhabdomyosarcoma
 UNPUBLISHED (2000)
 JOURNAL Contact: Friedman TB
 COMMENT Laboratory of Molecular Genetics
 National Institute on Deafness and Other Communication Disorders,
 National Institutes of Health
 5 Research Court, Room 2A-15, Rockville, MD 20850, USA
 Tel: 301 402 7580
 Fax: 301 496 7882
 Email: friedman@nidcd.nih.gov
 Plate: 02 row: 9 column: 09
 Seq primer: -21M13 forward primer (AB1)
 Classes: random plasmid subclone.
 Location/Qualifiers
 1..561
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="PAX3 CASTing Library 'ev'"
 /sex="Male"
 /lab_host="DH10B"
 /note="Vector: pGEM-T Easy; Human genomic DNA was partially digested with SmaI, ligated to ds linkers, and enriched for binding to human PAX3dQ+ protein using a whole genome PCR-based strategy. DNA fragments containing putative PAX3dQ+ binding sites were amplified by PCR and cloned into pGEM-T Easy (Promega). The ligation products were transformed into DH10B electrocompetent cells (Life Technologies)."

BASE COUNT 126 a 149 c 152 g 134 t
 ORIGIN

Query Match 80.9%: Score 17.8; DB 12; Length 561;
 Best Local Similarity 90.5%: Pred. No. 2.9e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgactgtgaacgctcgagatg 21
 |||||||
 DB 461 TGACTGTGAACGCTTAGATG 441

RESULT 3 BF971856 961 bp mRNA linear EST 22-JAN-2001
 LOCUS 602240444F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4328890 5',
 DEFINITION mRNA sequence.
 ACCESSION BF971856
 VERSION BF971856.1 GI:123339071
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 961)
 AUTHORS NIH-MGC http://mgc.ncl.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 UNPUBLISHED (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: AMCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.jnl.gov
 Plate: LLCM1189 row: h column: 11
 High quality sequence stop: 555.
 Location/Qualifiers
 1..961
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4328890"
 /clone_lib="NIH_MGC_46"
 /issue_type="telomysarcoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: uterus; Vector: pORF7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GCCACGAC(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the Laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."

BASE COUNT 205 a 225 c 240 g 291 t
 ORIGIN

Query Match 80.9%: Score 17.8; DB 10; Length 961;
 Best Local Similarity 90.5%: Pred. No. 3.4e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gactgtgaacgctcgagatga 22
 |||||||
 DB 650 GACTGTGAACGCTTCGGATGA 670

RESULT 4 A2060178 489 bp DNA linear GSS 30-MAR-2000
 LOCUS RPCI-23-405E23.TV RPCI-23 Mus musculus genomic clone RPCI-23-405E23
 DEFINITION , DNA sequence.
 ACCESSION A2060178
 VERSION A2060178.1 GI:7351427
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclurignathi; Muridae; Murinae; Mus.
 1 (bases 1 to 489)
 AUTHORS Zhao,S., Nierman,W., Feldblum,T., Malek,J., Shatsman,S., Akintet

BASE COUNT 126 a 149 c 152 g 134 t
 ORIGIN

TITLE
JOURNAL
COMMENT

, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSs: RPCI-23-405E23.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
7112 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208

Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pdejong@tigr.org, med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.html) or from Reseach Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
Plate: 405 row: E column: 23
Seq primer: Sp6
Class: BAC ends.

FEATURES
source

Location/Qualifiers
1. .483
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-405E23"
/clone_id="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site: 1; EORI: Site_2; EORI: Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT 162 a 198 t 198 t 198 t 198 t
ORIGIN

Query Match 79.1% Score 17.4; DB 12; Length 489;
Best Local Similarity 94.7% Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 tgactgtgaacgttcgaga 19
|||||
Db 170 TGACTGTGAACATTTCGAGA 152

RESULT 5
AZ886419/c 530 bp DNA linear GSS 05-MAR-2001
LOCUS RPCI-23-18216.TJ RPCI-23 Mus musculus genomic clone RPCI-23-18216,
DEFINITION DNA sequence.
ACCESSION AZ886419
VERSION AZ886419.1 GI:13205364
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 530)
Zhao, S., Nierman, W., Feldlyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
TITLE Mouse BAC End Sequences from Library RPCI-23
JOURNAL Unpublished (1999)
COMMENT Other GSSs: RPCI-23-18216.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA

FEATURES
source

Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pdejong@mail.chu.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.html). BAC end page: http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
Plate: 182 row: I column: 6
Seq primer: Sp6
Class: BAC ends.

Location/Qualifiers
1. .530
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-18216"
/clone_id="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site: 1; EORI: Site_2; EORI: Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT 174 a 65 c 73 g 218 t
ORIGIN

Query Match 79.1% Score 17.4; DB 12; Length 530;
Best Local Similarity 94.7% Pred. No. 4.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 tgactgtgaacgttcgaga 19
|||||
Db 189 TGACTGTGAACATTTCGAGA 171

RESULT 6
AQ245026 374 bp DNA linear GSS 03-OCT-1998
LOCUS HS_2056_B1_E03_MR CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate=2056 Col=5 Row=J, DNA sequence.
ACCESSION AQ245026
VERSION AQ245026.1 GI:3691600
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 374)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887

Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2056 row: J column: 5
Class: BAC ends
High quality sequence stop: 374.
Location/Qualifiers
1. .374

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Plate=2056 Col=5 Row=J"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/Note="Origin: sperm; Vector: pbeloBAC11; BAC Clones in
E-Coli DH10B"
BASE COUNT      91 a      73 c      92 g      117 t      1 others
ORIGIN

Query Match      78.2%; Score 17.2; DB 12; Length 374;
Best Local Similarity 86.4%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcgagatga 22
|||||
Db 207 TGACTGTGAACGATGTAGATGA 228

RESULT 7
AZ536502      408 bp      DNA      linear      GSS 03-NOV-2000
LOCUS      110300.96 Planococcus lllacinus DNA Planococcus lllacinus genomic,
DEFINITION      DNA sequence.
ACCESSION      AZ536502
VERSION      AZ536502.1 GI:11093449
KEYWORDS
SOURCE      GSS.
ORGANISM      lllac mealybug.
                Planococcus lllacinus
                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;
                Aphidiformes; Coccoidea; Pseudococcidae; Planococcus.
                1 (bases 1 to 408)
                Mohan, K.N. and Chandra, H.S.
                Mealybug shotgun sequencing
                Unpublished (2000)
                CONTACT: Mohan KN
                Microbiology and Cell Biology
                Indian Institute of Science
                Sir C.V. Raman Avenue, Bangalore, Karnataka 560012, India
                Email: mohan@cbl.iisc.ernet.in
                Class: shotgun.
FEATURES
    source      location/Qualifiers
                1..408
                /organism="Planococcus lllacinus"
                /db_xref="taxon:40930"
                /clone_lib="Planococcus lllacinus DNA"
BASE COUNT      134 a      83 c      80 g      111 t
ORIGIN

Query Match      78.2%; Score 17.2; DB 12; Length 408;
Best Local Similarity 86.4%; Pred. No. 4.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcgagatga 22
|||||
Db 251 TGACTGTGAACGATGTAGATGA 272

RESULT 8
BE723539      424 bp      mRNA      linear      EST 25-APR-2001
LOCUS      BE723539
DEFINITION      193384 MRC 4BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION      BE723539
VERSION      BE723539.1 GI:10124826
KEYWORDS      EST.
SOURCE      COW.
ORGANISM      Bos taurus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                Bovidae; Bovinae; Bos.

REFERENCE
    Smith T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
    Cassa, E., Wray, J.E., White, J., Cho, J., Fahnenkrug, S.C., Bennett
    G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Mckown, C.G.,
    Perlea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
    Keeler, J.W.
    Sequence evaluation of four pooled-tissue normalized bovine cDNA
    libraries and construction of a gene index for cattle
    Genome Res. 11 (4), 626-630 (2001)
JOURNAL
MEDLINE
COMMENT
    Contact: Smith TPL
    USDA, ARS, US Meat Animal Research Center
    PO Box 166, Clay Center, NE 68933-0166, USA
    Tel: 402 762 4366
    Fax: 402 762 4390
    Email: smith@email.marc.usda.gov
    Single pass sequencing. Bases called and alt_trimmed with phred
    v0.980904.e. Vector identified by cross_match with the -minscore 18
    and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCAGTCACGACG
Plate: 92 row: E column: 14
Seq primer: ATTTAGTGACACTATAG.
Location/Qualifiers
    1..424
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 4BOV"
/lissue_type="pooled"
/lab_host="DH10B"
/Note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 20 and day 40
embryos."
BASE COUNT      107 a      107 c      87 g      123 t
ORIGIN

Query Match      78.2%; Score 17.2; DB 10; Length 424;
Best Local Similarity 86.4%; Pred. No. 5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcgagatga 22
|||||
Db 268 TGACTGTGAACGATGTAGATGA 289

RESULT 9
AU083559      463 bp      mRNA      linear      EST 21-MAR-2000
LOCUS      AU083559
DEFINITION      AU083559 Rice green shoot Oryza sativa cDNA clone S14862, mRNA
                sequence.
ACCESSION      AU083559
VERSION      AU083559.1 GI:7274015
KEYWORDS
SOURCE      EST.
ORGANISM      Oryza sativa.
                Oryza sativa.
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                Ehrhartoideae; Oryzaceae; Oryza.
                1 (bases 1 to 463)
                Sasaki, T. and Yamamoto, K.
                Rice cDNA from green shoot (2000)
                Unpublished (2000)
                Contact: Takuji Sasaki
                National Institute of Agricultural Resources
                Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
                305-8602, Japan
                Tel: 81-298-38-7441
                Fax: 81-298-38-7468
                Email: tsasaki@agr.affrc.go.jp, URU:http://rgp.dna.affrc.go.jp/
                PROJECT "Rgp".
                S14862_62.

```

FEATURES
source

Location/Qualifiers
1. .463
/organism="Oryza sativa"
/strain="Nipponbare"
/db_xref="taxon:4530"
/clone_1lb="S14862"
/note="Rice green shoot"
/note="Green shoot (8 days old)"
BASE COUNT 151 a .74 c 109 g 127 t 2 others
ORIGIN

Query Match 78.2%; Score 17.2; DB 9; Length 463;
Best Local Similarity 86.4%; Pred. No. 5.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 151 TGAGTGTGAATGTTAGAGATGA 172

RESULT 10
LOCUS AU089685 479 bp mRNA linear EST 27-APR-2000
DEFINITION AU089685 Rice callus Oryza sativa cDNA clone C40060, mRNA sequence.
ACCESSION AU089685
VERSION AU089685.1 GI:7652165
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 479)
Sasaki,T. and Yamamoto,K.
Rice cDNA from callus (2000)
Unpublished (2000)
Contact: Takuji Sasaki
National Institute of Agricultural Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@agr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT="RGP",
CA0060_3%.

FEATURES
source

Location/Qualifiers
1. .479
/organism="Oryza sativa"
/strain="cultivar Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
/clone="C40060"
/clone_1lb="Rice callus"
/note="Vector: pBluescript II SK+; Site.1: SalI; Site.2:
NOTI; cDNA prepared from rice callus mRNAs by using
oligo(dT) as a primer and ligating to the SalI-NOTI site
of pBluescript II SK+ phagemid."
BASE COUNT 149 a 96 c 104 g 130 t
ORIGIN

Query Match 78.2%; Score 17.2; DB 9; Length 479;
Best Local Similarity 86.4%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 299 TGAGTGTGAATGTTAGAGATGA 320

RESULT 11
BJ094274 513 bp mRNA linear EST 12-DEC-2001
LOCUS BJ094274

DEFINITION BJ094274 NIBB Mochi normalized Xenopus early gastrula library
Xenopus laevis cDNA clone XL144P18 5', mRNA sequence.
ACCESSION BJ094274
VERSION BJ094274.1 GI:17594227
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 513)
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara
Y.

REFERENCE
AUTHORS Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers

FEATURES
source

1. .513
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL144P18"
/clone_1lb="NIBB Mochi normalized Xenopus early gastrula
library"
/issue_type="whole embryo"
/dev_stage="stage 10.5"
BASE COUNT 106 a 129 c 159 g 119 t
ORIGIN

Query Match 78.2%; Score 17.2; DB 10; Length 513;
Best Local Similarity 86.4%; Pred. No. 5.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 198 TGCCGTGAGACGCTGCCGATGA 219

RESULT 12
BJ796581 519 bp mRNA linear EST 02-OCT-2001
LOCUS BJ796581
DEFINITION H049FP08 Endosperm library from Oryza sativa (10 days after anthesis
) Oryza sativa cDNA clone H049FP08, mRNA sequence.
ACCESSION BJ796581
VERSION BJ796581.1 GI:15848305
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 519)
Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu
/H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.
A Gene Expression Screen in Oryza sativa
Unpublished (2001)
Contact: Dong HT
Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
Fax: 0086-571-86961525
Email: htdong@zjuem.zju.edu.cn
Seq primer: M13 forward primer.
Location/Qualifiers

FEATURES
source

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/db_xref="taxon:4530"
 /clone_lib="H049F08"
 /clone_lib="Endosperm library from Oryza sativa (10 days after anthesis)"
 /tissue_type="Endosperm"
 /dev_stage="10 days after anthesis"
 /note="Vector: psporf2"
 BASE COUNT 149 a 98 c 121 g 151 t

Query Match 78.2% Score 17.2: DB 10: Length 519;
 Best Local Similarity 86.4% Pred. No. 5.4e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcgagatga 22
 ||| ||||| ||| ||||| |||
 Db 266 TGAGTGTGAAGTGTAGAGATGA 287

RESULT 13
 BM037907

LOCUS S114c07 Stem library from Oryza sativa (3-5 leaf stage) Oryza
 DEFINITION sativa cDNA clone S114c07, mRNA sequence.
 ACCESSION BM037907
 VERSION BM037907.1 GI:16753528
 KEYWORDS EST.
 SOURCE Oryza sativa.
 ORGANISM Oryza sativa.

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 AUTHORS Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu
 1 (bases 1 to 571)
 A Gene Expression Screen in Oryza sativa
 Unpublished (2001)

TITLE Laboratory of Functional Genetics
 JOURNAL Bio-technology Institute of Zhejiang University
 COMMENT Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
 Tel: 0086-571-866892051
 Fax: 0086-571-86961525
 Email: htdong@zjuem.zju.edu.cn
 Seg primer: M13 forward primer.
 FEATURES Location/Qualifiers
 source 1..571

/organism="Oryza sativa"
 /db_xref="taxon:4530"
 /clone_lib="H049F08"
 /clone_lib="Stem library from Oryza sativa (3-5 leaf stage)"
 /tissue_type="Stem"
 /dev_stage="3-5 leaf stage"
 /note="Vector: psporf2"
 BASE COUNT 158 a 101 c 133 g 177 t 2 others

ORIGIN

Query Match 78.2% Score 17.2: DB 10: Length 571;
 Best Local Similarity 86.4% Pred. No. 5.5e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcgagatga 22
 ||| ||||| ||| ||||| |||
 Db 179 TGAGTGTGAAGTGTAGAGATGA 200

RESULT 14
 CNS05PD9 972 bp DNA linear GSS 26-MAY-2000
 LOCUS tetradon nigroviridis genome survey sequence T7 end of clone
 DEFINITION

005F08 of library A from Tetradon nigroviridis, genomic survey
 sequence.
 AL347814
 AL347814.1 GI:8241584
 GSS; genome survey sequence.
 Tetradon nigroviridis.
 Tetradon nigroviridis
 Tetradon nigroviridis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetradontiformes;
 Tetradontidae; Tetradon.
 1 (bases 1 to 972)
 Roest-Crollius,H., Tallon,O., Dasilva,C., Fitzames,C., Fisher,C.,
 Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
 Weissenbach,J.
 Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetradon nigroviridis
 Unpublished
 2 (bases 1 to 972)
 Roest-Crollius,H., Tallon,O., Dasilva,C., Bouneau,L., Fisher,C.,
 Bernot,A., Fitzames,C., Winkler,P., Brotlier,P., Quetier,F.,
 Saurin,W. and Weissenbach,J.
 Human gene number estimate provided by genome wide analysis using
 Tetradon nigroviridis DNA sequence
 Unpublished
 3 (bases 1 to 972)
 Genoscope.
 Direct Submission
 Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
 This sequence is a single read and was generated as part of a large
 scale clone-end sequencing project of the Tetradon nigroviridis
 genome. For more information, please take a look at
 http://www.genoscope.cns.fr/Tetradon.
 Location/Qualifiers
 1 972

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BASE COUNT 195 a 268 c 199 g 297 t 13 others

ORIGIN

Query Match 78.2% Score 17.2: DB 12: Length 972;
 Best Local Similarity 86.4% Pred. No. 6.7e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 tgactgtgaacgttcgagatga 22
 ||| ||||| ||| ||||| |||
 Db 46 TGCGTGTGAAGTGTAGAGATGA 25

RESULT 15
 AA094019
 LOCUS AA094019 105 bp mRNA linear EST 25-OCT-1996
 DEFINITION c11619.seq.F Human fetal heart, lambda zap Express Homo sapiens
 CDNA 5', mRNA sequence.
 ACCESSION AA094019
 VERSION AA094019.1 GI:1639612
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 105)
 Ilew,C.C.
 cDNAs from fetal heart (1996)
 Unpublished (1996)
 CONTACT: Ilew CC
 Brigham and Women's Hospital
 Harvard Medical School
 75 Francis St. Boston, MA 02115, USA

Tel: 6177328915
Fax: 6179750995

Email: cleveland@rics.bwh.harvard.edu

PCR Primers

FORWARD: 5' GCCAAGCTCGAATTAACCCCTCCTAATAAGGG 3'

BACKWARD: 5' CCAGTGAATTTGTAATACCGACTCCTATATAGGGCG 3'

Seq primer: 5' GAAATTAACTCCCTCACTAAAGGG 3'

FEATURES

source
1..105
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="human fetal heart, Lambda ZAP Express"
/lab_host="E. coli XL1-Blue"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
XhoI; mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a XhoI-Oligo dT
adaptor-primer. EcoRI adaptors were ligated, followed by
digestion with XhoI, for directional cloning into
predigested Lambda ZAP Express."
BASE COUNT 31 a 21 c 16 g 37 t
ORIGIN

Query Match 76.4%; Score 16.8; DB 9; Length 105;
Best Local Similarity 90.0%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 tgactgtgaacgttcgagat 20
|||||
Db 43 TGACTGTGAACCTTCAGAT 62

Search completed: September 3, 2002, 03:50:12
Job time: 5723 sec

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